

## GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND CORRELATION STUDIES F<sub>5</sub> FAMILIES IN RICE (*ORYZA SATIVA* L.)

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### ABSTRACT

*The present study was undertaken during kharif, 2015 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru on 42 F<sub>5</sub> families of rice belonging to four crosses along with five parents to study variability, heritability, genetic advance as per cent of mean and nature and direction of association among themselves and with grain yield. Data was recorded on seven characters which showed significant differences among themselves. Phenotypic and Genotypic coefficient of variation for grain yield and test weight is high compared to other traits. For traits days to 50% flowering, days to maturity and plant height, the heritability was high coupled with moderate genetic advance indicating the presence of both additive and non additive gene actions in governing the inheritance of these traits. Hence, exploitation of heterosis breeding for such traits will be effective. The study of character association revealed that panicle length showed significant positive association with grain yield per plant indicating that direct selection can be practiced for this character.*

**KEYWORDS:** Rice, F<sub>5</sub> Families, Variability, Heritability, Genetic Advance & Correlation

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### INTRODUCTION

Rice is the largest food crop in the world which meets the dietary needs of millions of people around the globe on a daily basis. Being a staple food for two thirds of the population, rice crop plays a pivotal role in the economy of the country. Andhra Pradesh is an important state contributing to the rice basket of the country with an area of 3.80 million hectares and a production of 11.56 million with a productivity of 3244 kg/ha. Population growth is accelerating at a rate of 1.8% because of which rice requirement would be 140 million tons by 2020 (Anonymous, 2013).

Demand for rice is increasing day by day and keeping in view of the future demand of rice as a food for human, there is a continuous need to evolve new varieties, which should exceed the yields of existing ones. Nature and magnitude of the total variability present plays a key role in the success of the breeding programme. Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) gives information on nature and magnitude of variation present in a population. Broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and is used as a predictive role in selection procedures (Allard, 1960). Estimation of heritability alone will not be of much use as it will not be of much use as it will measure only the additive and non additive gene action. Heritability estimates along with genetic advance

are more helpful in predicting gain under selection than heritability estimates alone (Johnson *et al.*, 1955).

To know how the improvement of one character will bring simultaneous improvement in other characters, study of correlations is essential for a plant breeder. The knowledge on the correlation between dependent variable like yield with different independent variables is essential for selection of the plants. To fulfill the objectives of the breeding programme, there should be sufficient variability among the studied genotypes. Also, determining the association between different traits is a prerequisite. The present study was therefore undertaken to study variability, heritability, genetic advance as percent of mean and nature and direction of association among themselves and with grain yield that helps in selection of superior genotypes.

## MATERIAL AND METHODS

The experimental material consisted of forty two F<sub>5</sub> families belonging to four crosses of rice with five parents obtained from Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru. All the genotypes along with their parents were evaluated in a randomized block design. Details of studied crosses were presented in table 1 and a detail of studied plant material was presented in table 2. All the package of practices were followed to raise a healthy crop. The data was recorded on five randomly selected plants from each entry pertaining to the traits plant height, number of panicles per plant, panicle length, grain yield per plant and test weight while for the traits days to 50% flowering and days to maturity the data was recorded on per pot basis. The mean values over two replications were used for statistical analysis and analysis was done as per Panse and Sukhatme (1985), Burton and Devane (1953), Johnson *et al.* (1955) and Falconer (1964).

## RESULTS AND DISCUSSIONS

The ANOVA studied revealed that sufficient variability existed among all the traits studied (Table 3). Comparing the values of GCV with PCV helps in determining the role of environmental factors (Table 4 and Figure 1). The PCV and GCV values are high for the traits grain yield and test weight when compared to other traits which indicates that there is high variability for both these traits. The extent of variability is moderate for the traits number of panicles per plant and panicle length, which is evident by moderate values of PCV and GCV while the variability is low for the traits days to 50% flowering, days to maturity and plant height. These results were in conformity with the findings of Sameera *et al.* (2015), Shrivastava *et al.* (2014), Patel *et al.* (2014), Paikhomba *et al.* (2014), Khare *et al.* (2014), Gangashetty *et al.* (2013) and Aditya and Bhartiya (2013).

For the traits, days to 50% flowering, days to maturity and plant height, high heritability coupled with moderate genetic advance as percent of mean was observed. Hence for the improvement of these traits, heterosis breeding will be more useful. High heritability coupled with low genetic advance was reported for number of panicles per plant, panicle length, grain yield per plant and test weight indicating the presence of non additive gene action and hence simple selection for these traits would not be effective. Similar results were reported by Sameera *et al.* (2015), Patel *et al.* (2014), Paikhomba *et al.* (2014), Aditya and Bhartiya (2013) and Hasan *et al.* (2011).

The correlation studies (Table 5 and Figure 1&2) revealed that there is a significant and positive correlation between panicle length and grain yield per plant (0.426\*/0.492\*). Hence direct selection can be used for that trait. Increase in the duration will decrease the yield which is evident by the negative correlation of grain with days to 50% flowering (-0.302\*/-0.318\*) and days to maturity (-0.364\*/-0.383\*). The influence of the characters plant height (-0.004/0.003) and

test weight (0.041/0.036) was low on the grain yield in the present study as they exhibit positive non significant correlations.

The association of days to 50% flowering is significant and positive with days to maturity (0.936\*/0.952\*), plant height (0.267\*/0.278\*) and number of panicles per plant (0.422\*/0.457\*) while the correlation between days to maturity with plant height (0.268\*/0.272\*) and number of panicles (0.370\*/0.413\*) is also positive and significant.

There is a significant correlation between plant height and number of panicles per plant (0.210\*/0.210\*) at both genotypic and phenotypic levels. At genotypic level, there is a positive significant correlation between number of panicles per plant and panicle length (0.2025/0.213\*) but the association of number of panicles per plant is negative and significant with test weight (-0.381\*/-0.431\*) at both phenotypic and genotypic levels. Strong positive association among the traits indicated that simultaneous selection for these characters would result in improvement of high yielding varieties. These results are in agreement with the findings of Jambhulkar and Bose (2014), Khare *et al.* (2014) and Patel *et al.* (2014). From the present study it can be envisaged that there is less environmental influence as the genotypic correlation values were higher when compared to phenotypic correlation values.

Thus the trait, panicle length, can be exploited as an important criterion in the selection programmes for the yield improvement.

## REFERENCES

1. Aditya J P and Bhartiya A. (2013). Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice in uttarakhand hills. *Journal of Rice Research*. 6 (2): 24-34.
2. Allard R W. (1960). *Principles of Plant Breeding*. John Wiley and Sons Inc., New York. 145-147 pp.
3. Burton G W and Devane E W. (1953). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clone material. *Agronomy Journal*. 45: 478-481.
4. Falconer D S. (1964). *An Introduction to Quantitative Genetics*. Oliver and Boyd, Edinburgh, London. 312-324 pp.
5. Gangashetty P I, Salimath P M and Hanamaratti N G. (2013). Genetic variability studies in genetically diverse non-basmati local aromatic genotypes of rice (*Oryza sativa* L.). *Rice Genomics and Genetics*. 4 (2): 4-8.
6. Hasan, M.J., Kulsum, M.U., Akter, A., Masuduzzaman, A.S.M and Ramesha, M.S. (2011). Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa* L.). *Bangladesh Journal of Plant Breeding and Genetics*. 24 (1): 45-51.
7. Jambhulkar N N, and Bose L K. (2014). Genetic variability and association of yield attributing traits with grain yield in upland rice. *Genetika*. 46 (3): 831-838.
8. Johnson H W, Robinson H F and Comstock R E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.
9. Khare R, Singh A K, Eram S and Singh, P K. (2014). Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L.). *SAARC Journal of Agriculture*. 12 (2): 40-51.
10. Paikhomba N, Arvind K, Chaurasia A K and Rai P K. (2014). Assessment of genetic parameters for yield and yield components in hybrid rice and parents. *Journal of Rice Research*. 2: 1-3.

11. Panse V G and Sukhatme P V. (1961). *Statistical methods for agricultural workers*. Indian Council of Agricultural Research, New Delhi. 242-246 pp.
12. Patel J R, Saiyad M R, Prajapati K N, Patel R A and Bhavani R T. (2014). Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 5 (3): 531-537.
13. Sameera S K, Prasanna Rajesh A, Jayalakshmi V, Nirmala P J and Srinivas T. (2015). Genetic variability studies for yield and yield componenets in rice (*Oryza sativa* L.). *Electroic Journal of Plant Breeding*. 6(1): 269-273.
14. Shrivastava A, Mishra D K, Koutu G K and Singh S K. (2014). Heritability and genetic advance estimation from parental lines of hybrid rice. *International Journal of Scientific Research*. 3(7): 11-13.

## APPENDICES

**Table 1: List of Crosses Studied and Number of Families Studied under Each Cross**

Cross	Number of Families Studied
MTU 7029/ MTU 1081	28
MTU 7029/ JGL 11118	2
MTU 7029/ NLR 34449	10
MTU 7029/ MTU 1121	2
<b>Total - Six Crosses</b>	<b>42</b>

**Table 2: List of F<sub>5</sub> Families Studied**

S. No	ENTRY	Cross Combination
1	MTU 2462-2-2-1	MTU 7029/ MTU 1081
2	MTU 2462-4-1-2	MTU 7029/ MTU 1081
3	MTU 2462-5-2-1	MTU 7029/ MTU 1081
4	MTU 2462-5-3-1	MTU 7029/ MTU 1081
5	MTU 2462-12-1-2	MTU 7029/ MTU 1081
6	MTU 2462-12-2-2	MTU 7029/ MTU 1081
7	MTU 2462-13-1-1	MTU 7029/ MTU 1081
8	MTU 2462-13-1-2	MTU 7029/ MTU 1081
9	MTU 2462-13-2-1	MTU 7029/ MTU 1081
10	MTU 2462-13-3-1	MTU 7029/ MTU 1081
11	MTU 2462-13-4-1	MTU 7029/ MTU 1081
12	MTU 2462-15-2-2	MTU 7029/ MTU 1081
13	MTU 2462-16-1-1	MTU 7029/ MTU 1081
14	MTU 2462-18-2-1	MTU 7029/ MTU 1081
15	MTU 2462-21-2-1	MTU 7029/ MTU 1081
16	MTU 2462-21-4-1	MTU 7029/ MTU 1081
17	MTU 2462-22-3-2	MTU 7029/ MTU 1081
18	MTU 2462-22-3-3	MTU 7029/ MTU 1081
19	MTU 2462-23-1-1	MTU 7029/ MTU 1081
20	MTU 2462-23-2-1	MTU 7029/ MTU 1081
21	MTU 2462-26-2-1	MTU 7029/ MTU 1081
22	MTU 2462-26-4-1	MTU 7029/ MTU 1081
23	MTU 2462-27-1-1	MTU 7029/ MTU 1081
24	MTU 2462-28-1-1	MTU 7029/ MTU 1081
25	MTU 2462-32-3-1	MTU 7029/ MTU 1081
26	MTU 2462-33-2-1	MTU 7029/ MTU 1081
27	MTU 2462-42-2-2	MTU 7029/ MTU 1081
28	MTU 2462-45-1-1	MTU 7029/ MTU 1081
29	MTU 2463-4-1-1	MTU 7029/ JGL 11118
30	MTU 2463-4-2-2	MTU 7029/ JGL 11118
31	MTU 2465-3-1-1	MTU 7029/ NLR 34449

Table 2: Contd.,		
32	MTU 2465-11-2-1	MTU 7029/ NLR 34449
33	MTU 2465-12-2-1	MTU 7029/ NLR 34449
34	MTU 2465-16-1-1	MTU 7029/ NLR 34449
35	MTU 2465-16-2-2	MTU 7029/ NLR 34449
36	MTU 2465-22-3-1	MTU 7029/ NLR 34449
37	MTU 2465-23-1-1	MTU 7029/ NLR 34449
38	MTU 2465-24-3-1	MTU 7029/ NLR 34449
39	MTU 2465-27-1-1	MTU 7029/ NLR 34449
40	MTU 2465-35-2-1	MTU 7029/ NLR 34449
41	MTU 2466-3-4-1	MTU 7029/ MTU 1121
42	MTU 2466-4-4-1	MTU 7029/ MTU 1121
		<b>PARENTS</b>
43		MTU 7029
44		MTU 1081
45		MTU 1121
46		JGL 11118
47		NLR 34449

**Table 3: Analysis of Variance (Mean Sum of Squares) for 10 Characters for 121 Genotypes of Rice (*Oryza sativa L.*) during Kharif, 2015**

Source of Variations	d. f.	Days to 50% Flowering	Days to Maturity	Plant Height	No. of Panicles per Plant	Panicle Length	Grain Yield per Plant	Test Weight
Mean Sum of Squares								
Replications	1	0.26	0.01	3.64	0.01	1.55	0.40	0.82
Genotypes	46	91.83*	92.51*	68.50*	4.71*	9.09*	38.95*	31.65*
Error	46	1.78	1.51	2.57	0.40	0.93	1.06	0.63

\*Significance at 5% level

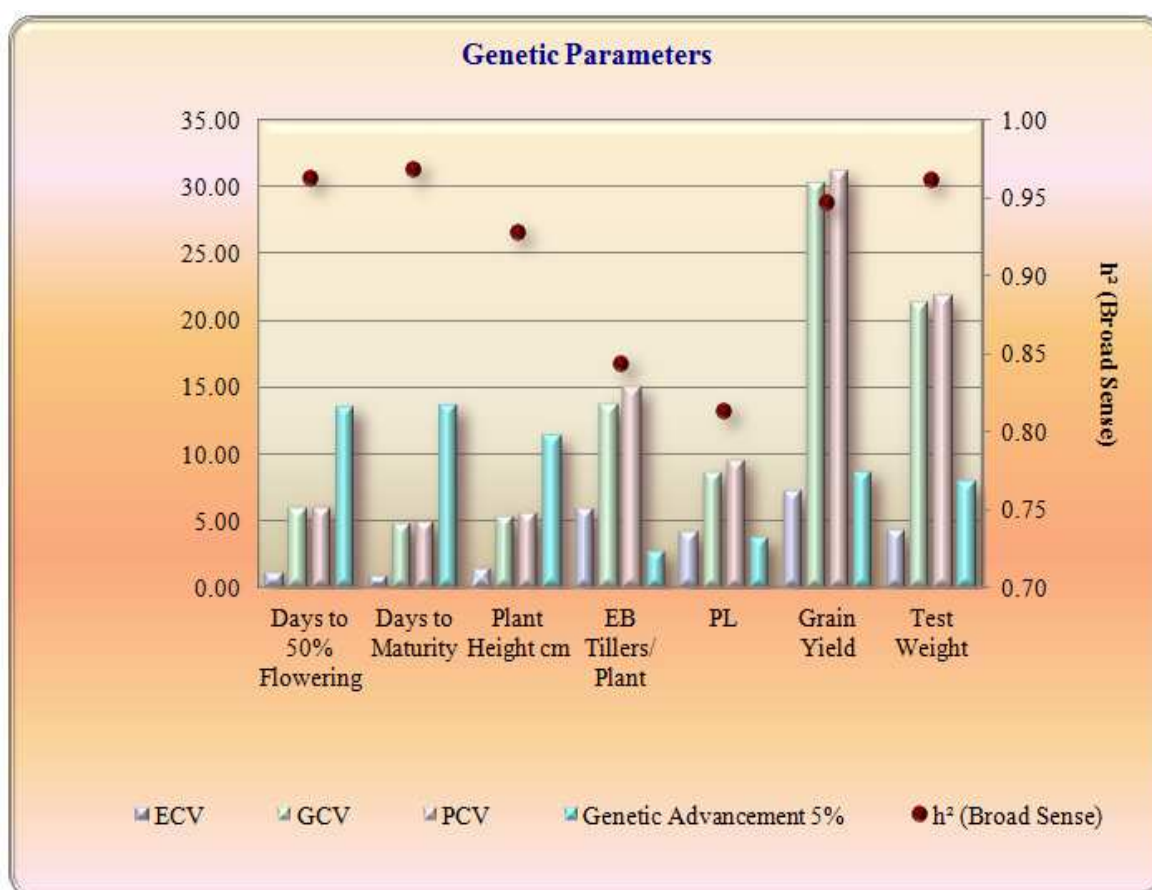
**Table 4: Estimates of Genetic Variability Parameters of Yield and Yield Component Attributes in Rice (*Oryza sativa L.*) during Kharif, 2015**

S. No	Character	Variability Parameters		$h^2$ (bs)	GAM
		PCV	GCV		
1	Days to 50% flowering	6.106	5.988	96.2	13.556
2	Days to maturity	4.961	4.881	96.8	13.671
3	Plant height (cm)	5.594	5.387	92.8	11.391
4	Number of panicles per plant	15.021	13.791	84.3	2.778
5	Panicle length (cm)	9.597	8.654	81.3	3.751
6	Grain yield per plant (cm)	31.151	30.312	94.7	8.725
7	Test weight (g)	21.418	21.418	96.1	7.953

**Table 5: Phenotypic and Genotypic Correlation Coefficient of 47 Lines  
(42 F<sub>5</sub> Families and 5 Parents) of Rice (*Oryza sativa* L.) during Kharif, 2015**

S. No	Characters		Days to 50% Flowering	Days to Maturity	Plant Height	Number of Panicles per Plant	Panicle Length	Test Weight
1.	Days to 50% flowering	P	1.0000					
		G	1.0000					
2.	Days to maturity	P	0.936*	1.0000				
		G	0.952*	1.0000				
3.	Plant height	P	0.267*	0.268*	1.0000			
		G	0.278*	0.272*	1.0000			
4.	Number of panicles per plant	P	0.422*	0.370*	0.210*	1.0000		
		G	0.457*	0.413*	0.210*	1.0000		
5.	Panicle length	P	-0.058	-0.065	0.198	0.2025	1.0000	
		G	-0.083	-0.095	0.216	0.213*	1.0000	
6.	Test weight	P	0.096	0.166	0.01	-0.381*	-0.016	1.0000
		G	0.100	0.174	0.014	-0.431*	-0.026	1.0000
7.	Grain yield per plant	P	-0.302*	-0.364*	-0.004	-0.106	0.426*	0.041
		G	-0.318*	-0.383*	0.003	-0.138	0.492*	0.036

\*Significance at 5% level

**Figure 1: Estimation of Genetic Parameters**

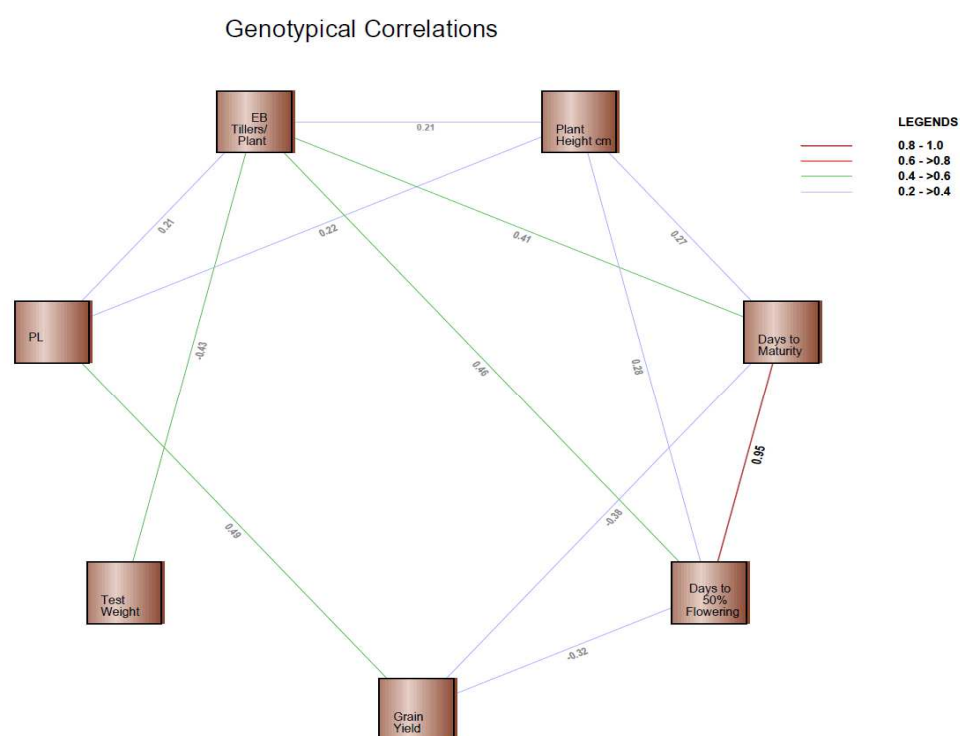


Figure 2: Genotypic Correlation Matrix

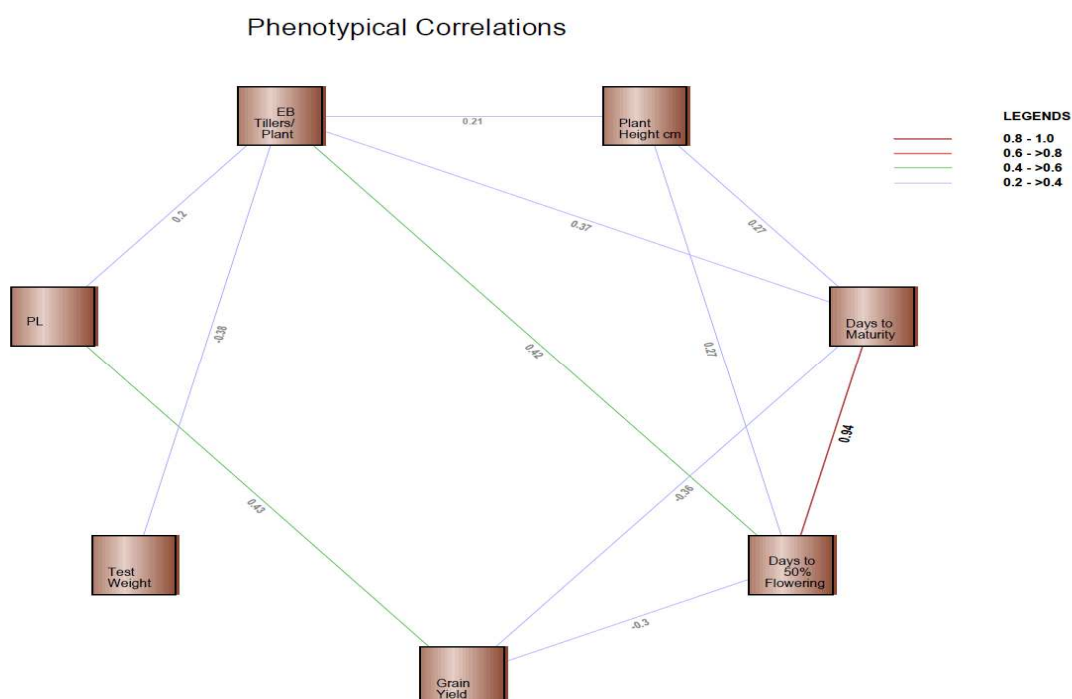


Figure 3: Phenotypic Correlation Matrix

